

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/044,205

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

SEQUENCE LISTING



<110> KAPPELLER-LIBERMANN, Rosana
BANDARU, Rajasekhar

<120> 69087, 15821, and 15418, Methods and Compositions of Human Proteins and Uses Thereof

<130> 10147-52U1

<140> 10/044,205

<141> 2001-10-22

<150> US 60/242,428

<151> 2000-10-23

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<151> 2000-10-20

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<160> 44

<170> PatentIn version 3.1

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COPY

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 <212> PRT
 <213> Homo sapiens

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35 40 45

Arg Gln Lys Leu Ser Leu Asn Phe His Ser Leu Cys Glu Gln Gln Pro
50 55 60

Ile Gly Arg Arg Leu Phe Arg Asp Phe Leu Ala Thr Val Pro Thr Phe
65 70 75 80

Arg Lys Ala Ala Thr Phe Leu Glu Asp Val Gln Asn Trp Glu Leu Ala
85 90 95

Glu Glu Gly Pro Thr Lys Asp Ser Ala Leu Gln Gly Leu Val Ala Thr
100 105 110

Cys Ala Ser Ala Pro Ala Pro Gly Asn Pro Gln Pro Phe Leu Ser Gln
115 120 125

Ala Val Ala Thr Lys Cys Gln Ala Ala Thr Thr Glu Glu Arg Val
130 135 140

Ala Ala Val Thr Leu Arg Lys Ala Glu Ala Met Ala Phe Leu Gln Glu
145 150 155 160

Gln Pro Phe Lys Asp Phe Val Thr Ser Ala Phe Tyr Asp Lys Phe Leu
165 170 175

Gln Trp Lys Leu Phe Glu Met Gln Pro Val Ser Asp Lys Tyr Phe Thr
180 185 190

Glu Phe Arg Val Leu Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Val
195 200 205

Gln Val Lys Asn Thr Gly Lys Met Tyr Ala Cys Lys Lys Leu Asp Lys
210 215 220

Lys Arg Leu Lys Lys Lys Gly Gly Glu Lys Met Ala Leu Leu Glu Lys

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Ala Phe Glu Ser Lys Thr His Leu Cys Leu Val Met Ser Leu Met Asn	260	265	270
Gly Gly Asp Leu Lys Phe His Ile Tyr Asn Val Gly Thr Arg Gly Leu	275	280	285
Asp Met Ser Arg Val Ile Phe Tyr Ser Ala Gln Ile Ala Cys Gly Met	290	295	300
Leu His Leu His Glu Leu Gly Ile Val Tyr Arg Asp Met Lys Pro Glu	305	310	315
Asn Val Leu Leu Asp Asp Leu Gly Asn Cys Arg Leu Ser Asp Leu Gly	325	330	335
Leu Ala Val Glu Met Lys Gly Gly Lys Pro Ile Thr Gln Arg Ala Gly	340	345	350
Thr Asn Gly Tyr Met Ala Pro Glu Ile Leu Met Glu Lys Val Ser Tyr	355	360	365
Ser Tyr Pro Val Asp Trp Phe Ala Met Gly Cys Ser Ile Tyr Glu Met	370	375	380
Val Ala Gly Arg Thr Pro Phe Lys Asp Tyr Lys Glu Lys Val Ser Lys	385	390	395
Glu Asp Leu Lys Gln Arg Thr Leu Gln Asp Glu Val Lys Phe Gln His	405	410	415
Asp Asn Phe Thr Glu Glu Ala Lys Asp Ile Cys Arg Leu Phe Leu Ala	420	425	430
Lys Lys Pro Glu Gln Arg Leu Gly Ser Arg Glu Lys Ser Asp Asp Pro	435	440	445
Arg Lys His His Phe Phe Lys Thr Ile Asn Phe Pro Arg Leu Glu Ala	450	455	460

Gly Leu Ile Glu Pro Pro Phe Val Pro Asp Pro Ser Val Val Tyr Ala
 465 470 475 480

Lys Asp Ile Ala Glu Ile Asp Asp Phe Ser Glu Val Arg Gly Val Glu
 485 490 495

Phe Asp Asp Lys Asp Lys Gln Phe Phe Lys Asn Phe Ala Thr Gly Ala
 500 505 510

Val Pro Ile Ala Trp Gln Glu Glu Ile Ile Glu Thr Gly Leu Phe Glu
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 <212> DNA
 <213> Homo sapiens

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35 40 45

Arg Gln Lys Leu Ser Leu Asn Phe His Ser Leu Cys Glu Gln Gln Pro
50 55 60

Ile Gly Arg Arg Leu Phe Arg Asp Phe Leu Ala Thr Val Pro Thr Phe
65 70 75 80

Arg Lys Ala Ala Thr Phe Leu Glu Asp Val Gln Asn Trp Glu Leu Ala
85 90 95

Glu Glu Gly Pro Thr Lys Asp Ser Ala Leu Gln Gly Leu Val Ala Thr
100 105 110

Cys Ala Ser Ala Pro Ala Pro Gly Asn Pro Gln Pro Phe Leu Ser Gln
115 120 125

Ala Val Ala Thr Lys Cys Gln Ala Ala Thr Thr Glu Glu Glu Arg Val
130 135 140

Ala Ala Val Thr Leu Ala Lys Ala Glu Ala Met Ala Phe Leu Gln Glu
145 150 155 160

Gln Pro Phe Lys Asp Phe Val Thr Ser Ala Phe Tyr Asp Lys Phe Leu
165 170 175

Gln Trp Lys Leu Phe Glu Met Gln Pro Val Ser Asp Lys Tyr Phe Thr
180 185 190

Glu Phe Arg Val Leu Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Val
195 200 205

Gln Val Lys Asn Thr Gly Lys Met Tyr Ala Cys Lys Lys Leu Asp Lys
210 215 220

Lys Arg Leu Lys Lys Lys Gly Gly Glu Lys Met Ala Leu Leu Glu Lys
225 230 235 240

Glu Ile Leu Glu Lys Val Ser Ser Pro Phe Ile Val Ser Leu Ala Tyr
245 250 255

Ala Phe Glu Ser Lys Thr His Leu Cys Leu Val Met Ser Leu Met Asn
260 265 270

Gly Gly Asp Leu Lys Phe His Ile Tyr Asn Val Gly Thr Arg Gly Leu
275 280 285

Asp Met Ser Arg Val Ile Phe Tyr Ser Ala Gln Ile Ala Cys Gly Met
290 295 300

Leu His Leu His Glu Leu Gly Ile Val Tyr Arg Asp Met Lys Pro Glu
 305 310 315 320

Asn Gly Leu Leu Asp Asp Leu Gly Asn Cys Arg Leu Ser Asp Leu Gly
 325 330 335

Leu Ala Val Glu Met Lys Gly Gly Lys Pro Ile Thr Gln Arg Ala Gly
 340 345 350

Thr Asn Gly Tyr Met Ala Pro Glu Ile Leu Met Glu Lys Val Ser Tyr
 355 360 365

Ser Tyr Pro Val Asp Trp Phe Ala Met Gly Cys Ser Ile Tyr Glu Met
 370 375 380

Val Ala Gly Arg Thr Pro Phe Lys Asp Tyr Lys Glu Lys Val Ser Lys
 385 390 395 400

Glu Asp Leu Lys Gln Arg Thr Leu Gln Asp Glu Val Lys Phe Gln His
 405 410 415

Asp Asn Phe Thr Glu Glu Ala Lys Asp Ile Cys Arg Leu Phe Leu Ala
 420 425 430

Lys Lys Pro Glu Gln Arg Leu Arg Ser Arg Glu Lys Ser Asp Asp Pro
 435 440 445

Arg Lys His His Phe Phe Lys Thr Ile Asn Phe Pro Arg Leu Glu Ala
 450 455 460

Gly Leu Ile Glu Pro Pro Phe Val Pro Asp Pro Ser Val Val Tyr Ala
 465 470 475 480

Lys Asp Ile Ala Glu Ile Asp Asp Phe Ser Glu Val Arg Gly Val Glu
 485 490 495

Phe Asp Asp Lys Asp Lys Gln Phe Phe Lys Asn Phe Ala Thr Gly Ala
 500 505 510

Val Pro Ile Ala Trp Gln Glu Glu Ile Ile Glu Thr Gly Leu Phe Glu
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535

540

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<213> *Spermophilus tridecemlineatus*

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35 40 45

Ser Leu Ser Pro His Phe His Ser Leu Cys Glu Gln Gln Pro Ile Gly
50 55 60

Arg Arg Leu Phe Arg Asp Phe Leu Ala Thr Val Pro Lys Tyr Ser Gln
65 70 75 80

Ala Val Ala Phe Leu Glu Asp Val Gln Asn Trp Glu Leu Ala Glu Glu
85 90 95

Gly Pro Ala Lys Thr Ser Thr Leu Gln Gln Leu Ala Ala Thr Cys Ala
100 105 110

Arg Asp Pro Gly Pro Gln Ser Phe Leu Ser Gln Asp Leu Ala Thr Lys
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145 150 155 160

Phe Leu Ala Ser Pro Phe Tyr Asp Arg Phe Leu Gln Trp Lys Leu Phe
165 170 175

Glu Met Gln Pro Val Ser Asp Lys Tyr Phe Thr Glu Phe Arg Val Leu
180 185 190

Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Val Gln Val Arg Asn Thr
195 200 205

Gly Lys Met Tyr Ala Cys Lys Lys Leu Asp Lys Lys Arg Leu Lys Lys
210 215 220

Lys Gly Gly Glu Lys Met Ala Leu Leu Glu Lys Glu Ile Leu Glu Lys
225 230 235 240

Val Asn Ser Pro Phe Ile Val Ser Leu Ala Tyr Ala Phe Glu Ser Lys
245 250 255

Thr His Leu Cys Leu Val Met Ser Leu Met Asn Gly Gly Asp Leu Lys
260 265 270

Phe His Ile Tyr Asn Val Gly Thr Arg Gly Leu Ala Met Ser Arg Val
275 280 285

Ile Phe Tyr Thr Ala Gln Met Thr Cys Gly Val Leu His Leu His Gly
290 295 300

Leu Gly Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Val Leu Leu Asp
305 310 315 320

Asp Leu Gly Asn Cys Arg Leu Ser Asp Leu Gly Leu Ala Val Glu Val
325 330 335

Gln Asp Asp Lys Pro Ile Thr Gln Arg Ala Gly Thr Asn Gly Tyr Met
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Ala Pro Glu Ile Leu Met Asp Lys Ala Ser Tyr Ser Tyr Pro Val Asp
355 360 365

Trp Phe Ala Met Gly Cys Ser Ile Tyr Glu Met Val Ala Gly Arg Thr
370 375 380

Pro Phe Lys Asp Phe Lys Glu Lys Val Ser Lys Glu Asp Leu Lys Glu
385 390 395 400

Arg Thr Met Lys Asp Glu Val Ala Phe His His Glu Asn Phe Thr Glu
405 410 415

Glu Thr Lys Asp Ile Cys Arg Leu Phe Leu Ala Lys Lys Pro Glu Gln
420 425 430

Arg Leu Gly Ser Arg Glu Lys Ala Asp Asp Pro Arg Lys His Pro Phe
435 440 445

Phe Gln Thr Val Asn Phe Pro Arg Leu Glu Ala Gly Leu Val Glu Pro
450 455 460

Pro Phe Val Pro Asp Pro Ser Val Val Tyr Ala Lys Asp Val Asp Glu
465 470 475 480

Ile Asp Asp Phe Ser Glu Val Arg Gly Val Glu Phe Asp Asp Lys Asp
485 490 495

Lys Gln Phe Phe Gln Arg Phe Ser Thr Gly Ala Val Pro Val Ala Trp
500 505 510

Gln Glu Glu Ile Ile Glu Thr Gly Leu Phe Glu Glu Leu Asn Asp Pro
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Asn Arg Pro Ser Gly Asp Gly Lys Gly Asp Ser Ser Lys Ser Gly Val
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Cys Leu Leu Leu
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<212> PRT
<213> Oryzias latipes

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Ile Glu Lys Asp Phe Thr Leu Leu Cys Glu Arg Gln Pro Ile Gly Lys
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Arg Leu Phe Arg Asp Phe Leu Ala Asn Thr Pro Glu Phe Lys Leu Ala
65 70 75 80

Ala Glu Phe Leu Asp Glu Leu Tyr Asp Trp Asp Leu Ala Glu Gly Ala
85 90 95

Ala Lys Asp Lys Ala Arg Gln Asn Ile Ile Asn Lys Tyr Cys Lys Pro
100 105 110

Asp Ser Lys Thr Phe Leu Thr Phe Leu Ser Gly Glu Pro Ala Glu Lys
115 120 125

Cys Lys Ser Val Thr Asp Ala Thr Phe Glu Glu Val Met Lys Asn Lys
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Val Gln Asp Gly Val Arg Glu Phe Leu Lys Gly Lys Pro Phe Thr Glu
145 150 155 160

Tyr Gln Gly Ser Gln Tyr Phe Asp Lys Phe Leu Gln Trp Lys Glu Tyr
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Glu Lys Gln Pro Ile Ser Asp Lys Tyr Phe Tyr Glu Phe Arg Thr Leu
180 185 190

Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Val Gln Val Lys Asn Thr
195 200 205

Gly Gln Met Tyr Ala Cys Lys Lys Leu Cys Lys Lys Arg Leu Lys Lys
210 215 220

Lys Gly Gly Glu Lys Met Ala Leu Leu Glu Lys Gln Ile Leu Glu Lys
225 230 235 240

Val Asn Ser Leu Phe Leu Val Asn Leu Ala Tyr Ala Tyr Asp Thr Lys
245 250 255

Thr His Leu Cys Leu Val Met Thr Leu Met Asn Gly Gly Asp Leu Lys
260 265 270

Tyr His Ile Tyr Asn Ile Gly Tyr Asp Gly Lys Gly Val Asp Lys Gly
275 280 285

Ile Glu Met Lys Arg Ile Ile His Tyr Thr Ala Gln Ile Thr Thr Gly
290 295 300

Ile Leu His Leu His Asp Met Asp Ile Ile Tyr Arg Asp Met Lys Pro
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Glu Asn Val Leu Leu Asp Ser Gln Gly Gln Cys Arg Leu Ser Asp Leu
325 330 335

Gly Leu Ala Ile Glu Ile Ala Pro Gly Lys Thr Val Thr Gln Met Ala
340 345 350

Gly Thr Gly Ala Tyr Met Ala Pro Glu Ile Leu Ser Lys Thr Pro Tyr
355 360 365

Arg Thr Ser Val Asp Trp Trp Ala Leu Gly Cys Ser Ile Tyr Glu Met
370 375 380

Val Ala Gly Tyr Thr Pro Phe Lys Gly Pro Glu Ser Lys Lys Glu Lys
385 390 395 400

Val Glu Lys Glu Glu Val Gln Arg Arg Ile Leu Asn Glu Glu Pro Lys
405 410 415

Trp Glu His Lys Cys Phe Asp Ala Pro Thr Lys Asp Val Ile Gln Gln
420 425 430

Phe Leu Lys Lys Lys Ile Asp Glu Arg Leu Gly Met Arg Asn Asn Met
435 440 445

Glu Asp Pro Arg Lys His Glu Trp Phe Lys Ser Ile Asn Phe Pro Arg
450 455 460

Leu Glu Ala Gly Leu Val Asp Pro Pro Trp Val Pro Lys Pro Asn Val
465 470 475 480

Val Tyr Ala Lys Asp Thr Gly Asp Ile Ala Glu Phe Ser Glu Ile Lys
485 490 495

Gly Ile Glu Phe Asp Ala Lys Asp Asp Lys Phe Phe Lys Glu Phe Ser
500 505 510

Thr Gly Ala Val Pro Ile Gln Trp Gln Gln Glu Met Ile Glu Thr Gly
515 520 525

Leu Phe Asp Glu Leu Asn Asp Pro Asn Arg Lys Glu Gly Ala Gly Gly
530 535 540

Gly Asp Asp Glu Lys Lys Ser Gly Thr Cys Ala Leu Leu
545 550 555

<210> 14
<211> 549
<212> PRT
<213> *Cyprinus carpio*

<400> 14

Met Cys Asp Met Gly Gly Leu Asp Asn Leu Val Ala Asn Thr Ala Tyr
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Ser Leu Ser Leu Pro Lys Pro Glu Gln Cys Ala Ala Leu Arg Ser Thr
35 40 45

Leu Asp Lys Asp Phe Glu Ser Leu Cys Glu Lys Gln Pro Ile Gly Lys
50 55 60

Arg Phe Phe Arg Gln Tyr Leu Asp Gln Gly Gly Pro Glu Cys Asn Ala
65 70 75 80

Ala Ala Glu Phe Leu Asp Asp Leu Asn Asp Trp Glu Leu Ser Glu Ala
85 90 95

Ala Ala Lys Asp Lys Ala Arg Thr Asn Ile Ile Asn Lys Phe Cys Lys
100 105 110

Asp Gly Ser Lys Ser Ser Leu Thr Phe Leu Thr Gly Asp Val Ala Thr
115 120 125

Lys Cys Lys Ala Val Thr Asp Lys Asp Phe Glu Glu Val Met Gly Gln
130 135 140

Val Lys Glu Ala Thr Lys Glu Phe Leu Lys Gly Lys Pro Phe Thr Asp
 145 150 155 160

Tyr Gln Thr Ser Glu Phe Phe Glu Lys Phe Leu Gln Trp Lys Glu Tyr
 165 170 175

Glu Lys Gln Pro Ile Thr Glu Lys Tyr Phe Tyr Glu Phe Arg Thr Leu
 180 185 190

Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Val Gln Val Lys Asn Thr
 195 200 205

Gly Gln Met Tyr Ala Cys Lys Lys Leu Cys Lys Lys Arg Leu Lys Lys
 210 215 220

Lys His Gly Glu Lys Met Ala Leu Leu Glu Lys Lys Ile Leu Glu Lys
 225 230 235 240

Val Asn Ser Leu Phe Ile Val Ser Leu Ala Tyr Ala Tyr Asp Thr Lys
 245 250 255

Thr His Leu Cys Leu Val Met Ser Leu Met Asn Gly Gly Asp Leu Lys
 260 265 270

Tyr His Ile Tyr Asn Ile Gly Glu Lys Gly Ile Glu Met Glu Arg Ile
 275 280 285

Ile Tyr Tyr Thr Ala Gln Ile Thr Thr Gly Met Leu Gln Leu His Asn
 290 295 300

Met Asp Ile Val Tyr Arg Asp Met Lys Pro Glu Asn Val Leu Leu Asp
 305 310 315 320

Ser Gln Gly Gln Cys Arg Leu Ser Asp Leu Gly Leu Ala Val Glu Ile
 325 330 335

Pro Val Gly Lys Thr Thr Thr Gln Lys Ala Gly Thr Gly Ala Tyr Met
 340 345 350

Ala Pro Glu Ile Leu Thr Glu Thr Pro Tyr Arg Thr Ser Val Asp Trp
 355 360 365

Trp Ala Leu Gly Cys Ser Ile Tyr Glu Met Val Ala Gly Tyr Thr Pro
 370 375 380

Phe Lys Gly Pro Glu Ala Lys Lys Glu Lys Val Glu Lys Glu Glu Val
 385 390 395 400

Gln Arg Arg Ile Ile Asn Glu Glu Pro Lys Phe Glu His Lys Asn Phe
 405 410 415

Asn Ala Pro Thr Ile Asp Ile Ile Lys Gln Phe Leu Lys Lys Lys Ile
 420 425 430

Asp Glu Arg Leu Gly Cys Lys Gly Asp Asp Pro Arg Lys His Glu Trp
 435 440 445

Phe Lys Ser Ile Asn Phe Ala Arg Leu Glu Ala Gly Leu Ile Asp Pro
 450 455 460

Pro Trp Val Pro Lys Pro Asn Val Val Tyr Ala Lys Asp Thr Gly Asp
 465 470 475 480

Ile Ala Glu Phe Ser Glu Ile Lys Gly Ile Glu Phe Asp Ala Lys Asp
 485 490 495

Glu Lys Phe Phe Lys Glu Phe Ser Thr Gly Ala Val Ser Ile Ala Trp
 500 505 510

Gln Lys Glu Met Ile Asp Thr Gly Leu Phe Asp Glu Leu Asn Asp Pro
 515 520 525

Asn Arg Lys Glu Ser Ser Gly Gly Leu Asp Asp Asp Lys Lys Ser Gly
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Thr Cys Thr Leu Leu
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<210> 21
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 <212> DNA
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<212> PRT
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<400> 22

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Pro Val Cys Arg Gly Cys Val Asn Tyr Glu Gly Ala Asp Arg Ile Glu
35 40 45

Phe Val Ile Glu Thr Ala Arg Gln Leu Lys Arg Ala His Gly Cys Phe
50 55 60

Pro Glu Gly Arg Ser Pro Pro Gly Ala Ala Ala Ser Ala Ala Ala Lys
65 70 75 80

Pro Pro Pro Leu Ser Ala Lys Asp Ile Leu Leu Gln Gln Gln Gln Gln
85 90 95

Leu Gly His Gly Gly Pro Glu Ala Ala Pro Arg Ala Pro Gln Ala Leu
100 105 110

Glu Arg Tyr Pro Leu Ala Ala Ala Glu Arg Pro Pro Arg Leu Gly
115 120 125

Ser Asp Phe Gly Ser Ser Arg Pro Ala Ala Ser Leu Ala Gln Pro Pro
130 135 140

Thr Pro Gln Pro Pro Pro Val Asn Gly Ile Leu Val Pro Asn Gly Phe
145 150 155 160

Ser Lys Leu Glu Glu Pro Pro Glu Leu Asn Arg Gln Ser Pro Asn Pro
165 170 175

Arg Arg Gly His Ala Val Pro Pro Thr Leu Val Pro Leu Met Asn Gly
180 185 190

Ser Ala Thr Pro Ala Ala Ala Ser Leu Gly Ser Ala Gln Pro Thr Asp
195 200 205

Leu Gly Ala His Lys Arg Pro Ala Ser Val Ser Ser Ser Ala Ala Val
210 215 220

Glu His Glu Gln Arg Glu Ala Ala Ala Lys Glu Lys Gln Pro Pro Pro
225 230 235 240

Pro Ala His Arg Gly Pro Ala Asp Ser Leu Ser Thr Ala Ala Gly Ala
245 250 255

Ala Glu Leu Ser Ala Glu Gly Ala Gly Lys Ser Arg Gly Ser Gly Glu
260 265 270

Gln Asp Trp Val Asn Arg Pro Lys Thr Val Arg Asp Thr Leu Leu Ala
275 280 285

Leu His Gln His Gly His Ser Gly Pro Phe Glu Ser Lys Phe Lys Lys
290 295 300

Glu Pro Ala Leu Thr Ala Gly Arg Leu Leu Gly Phe Glu Ala Asn Gly
305 310 315 320

Ala Asn Gly Ser Lys Ala Val Ala Arg Thr Ala Arg Lys Arg Lys Pro
325 330 335

Ser Pro Glu Pro Glu Gly Glu Val Gly Pro Pro Lys Ile Asn Gly Glu
340 345 350

Ala Gln Pro Trp Leu Ser Thr Ser Thr Glu Gly Leu Lys Ile Pro Met
355 360 365

Thr Pro Thr Ser Ser Phe Val Ser Pro Pro Pro Pro Thr Ala Ser Pro
370 375 380

His Ser Asn Arg Thr Thr Pro Pro Glu Ala Ala Gln Asn Gly Gln Ser
385 390 395 400

Pro Met Ala Ala Leu Ile Leu Val Ala Asp Asn Ala Gly Gly Ser His
405 410 415

Ala Ser Lys Asp Ala Asn Gln Val His Ser Thr Thr Arg Arg Asn Ser
420 425 430

Asn Ser Pro Pro Ser Pro Ser Ser Met Asn Gln Arg Arg Leu Gly Pro
435 440 445

Arg Glu Val Gly Gly Gln Gly Ala Gly Asn Thr Gly Gly Leu Glu Pro
450 455 460

Val His Pro Ala Ser Leu Pro Asp Ser Ser Leu Ala Thr Ser Ala Pro
465 470 475 480

Leu Cys Cys Thr Leu Cys His Glu Arg Leu Glu Asp Thr His Phe Val
485 490 495

Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe Pro Cys Ser Arg
500 505 510

Gln Ser Ile Lys Gln Gln Gly Ala Ser Gly Glu Val Tyr Cys Pro Ser

Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro Trp Ala Phe Met
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Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val Lys Val Lys Lys
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Glu Arg Asp Ser

<210> 23

<211> 1692

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 27
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<210> 30
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<212> DNA
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<400> 30
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<210> 31
<211> 796
<212> PRT
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<400> 31

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Cys Asp Leu Pro Arg Met Pro Trp Ala Met Ile Trp Asp Phe Ser Glu
20 25 30

Pro Val Cys Arg Gly Cys Val Asn Tyr Glu Gly Ala Asp Arg Ile Glu
35 40 45

Phe Val Ile Glu Thr Ala Arg Gln Leu Lys Arg Ala His Gly Cys Phe
50 55 60

Gln Asp Gly Arg Ser Pro Gly Pro Pro Pro Pro Val Gly Val Lys Thr
65 70 75 80

Val Ala Leu Ser Ala Lys Glu Ala Ala Ala Ala Ala Ala Ala Ala
85 90 95

Ala Ala Ala Ala Ala Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln
100 105 110

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu
 115 120 125

Asn His Val Asp Gly Ser Ser Lys Pro Ala Val Leu Ala Ala Pro Ser
 130 135 140

Gly Leu Glu Arg Tyr Gly Leu Ser Ala Ala Ala Ala Ala Ala Ala
 145 150 155 160

Ala Ala Ala Ala Val Glu Gln Arg Ser Arg Phe Glu Tyr Pro Pro Pro
 165 170 175

Pro Val Ser Leu Gly Ser Ser Ser His Thr Ala Arg Leu Pro Asn Gly
 180 185 190

Leu Gly Gly Pro Asn Gly Phe Pro Lys Pro Thr Pro Glu Glu Gly Pro
 195 200 205

Pro Glu Leu Asn Arg Gln Ser Pro Asn Ser Ser Ser Ala Ala Ala Ser
 210 215 220

Val Ala Ser Arg Arg Gly Thr His Gly Gly Leu Val Thr Gly Leu Pro
 225 230 235 240

Asn Pro Gly Gly Gly Gly Gly Pro Gln Leu Thr Val Pro Pro Asn Leu
 245 250 255

Leu Pro Gln Thr Leu Leu Asn Gly Pro Ala Ser Ala Ala Val Leu Pro
 260 265 270

Pro Pro Pro Pro His Ala Leu Gly Ser Arg Gly Pro Pro Thr Pro Ala
 275 280 285

Pro Pro Gly Ala Pro Gly Gly Pro Ala Cys Leu Gly Gly Thr Pro Gly
 290 295 300

Val Ser Ala Thr Ser Ser Ser Ala Ser Ser Ser Thr Ser Ser Ser Val
 305 310 315 320

Ala Glu Val Gly Val Gly Ala Gly Gly Lys Arg Pro Gly Ser Val Ser
 325 330 335

Ser Thr Asp Gln Glu Arg Glu Leu Lys Glu Lys Gln Arg Asn Ala Glu

340

345

350

Ala Leu Ala Glu Leu Ser Glu Ser Leu Arg Asn Arg Ala Glu Glu Trp
 355 360 365

Ala Ser Lys Pro Lys Met Val Arg Asp Thr Leu Leu Thr Leu Ala Gly
 370 375 380

Cys Thr Pro Tyr Glu Val Arg Phe Lys Lys Asp His Ser Leu Leu Gly
 385 390 395 400

Arg Val Phe Ala Phe Asp Ala Val Ser Lys Pro Gly Met Asp Tyr Glu
 405 410 415

Leu Lys Leu Phe Ile Glu Tyr Pro Thr Gly Ser Gly Asn Val Tyr Ser
 420 425 430

Ser Ala Ser Gly Val Ala Lys Gln Met Tyr Gln Asp Cys Met Lys Asp
 435 440 445

Phe Gly Arg Gly Leu Ser Ser Gly Phe Lys Tyr Leu Glu Tyr Glu Lys
 450 455 460

Lys His Gly Ser Gly Asp Trp Arg Leu Leu Gly Asp Leu Leu Pro Glu
 465 470 475 480

Ala Val Arg Phe Phe Lys Glu Gly Val Pro Gly Ala Asp Met Leu Pro
 485 490 495

Gln Pro Tyr Leu Asp Ala Ser Cys Pro Met Leu Pro Thr Ala Leu Val
 500 505 510

Ser Leu Ser Arg Ala Pro Ser Ala Pro Pro Gly Thr Gly Ala Leu Pro
 515 520 525

Pro Ala Ala Pro Ser Gly Arg Gly Ala Ala Ala Ser Leu Arg Lys Arg
 530 535 540

Lys Ala Ser Pro Glu Pro Pro Asp Ser Ala Glu Gly Ala Leu Lys Leu
 545 550 555 560

Gly Glu Glu Gln Gln Arg Gln Gln Trp Met Ala Asn Gln Ser Glu Ala
 565 570 575

Leu Lys Leu Thr Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala
580 585 590

Ala Gly Gly Pro Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn
595 600 605

Arg Thr Thr Pro Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met
610 615 620

Ala Ala Leu Met Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro
625 630 635 640

Lys Asp Gly Ser Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn
645 650 655

Ser Ser Ser Pro Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu
660 665 670

Ala Ser Arg Asn Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Pro
675 680 685

Ser Ala His Pro Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp
690 695 700

Ser Pro Met Ala Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu
705 710 715 720

Arg Leu Glu Asp Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His
725 730 735

Lys Phe Cys Phe Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala
740 745 750

Thr Gly Glu Val Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly
755 760 765

Ser Asn Val Pro Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu
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Ala Gly Asp Val Lys Val Lys Lys Glu Arg Asp Pro
785 790 795

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<212> PKT
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<400> 32

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Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
35 40 45

Gln Gln Gln Gln Gln Gln Leu Asn His Val Asp Gly Ser Ser Lys Pro
50 55 60

Ala Val Leu Ala Ala Pro Ser Gly Leu Glu Arg Tyr Gly Leu Ser Ala
65 70 75 80

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Val Glu Gln Arg Ser
85 90 95

Arg Phe Glu Tyr Pro Pro Pro Pro Val Ser Leu Gly Ser Ser Ser His
100 105 110

Thr Ala Arg Leu Pro Asn Gly Leu Gly Gly Pro Asn Gly Phe Pro Lys
115 120 125

Pro Thr Pro Glu Glu Gly Pro Pro Glu Leu Asn Arg Gln Ser Pro Asn
130 135 140

Ser Ser Ser Ala Ala Ala Ser Val Ala Ser Arg Arg Gly Thr His Gly
145 150 155 160

Gly Leu Val Thr Gly Leu Pro Asn Pro Gly Gly Gly Gly Gly Pro Gln
165 170 175

Leu Thr Val Pro Pro Asn Leu Leu Pro Gln Thr Leu Leu Asn Gly Pro
180 185 190

Ala Ser Ala Ala Val Leu Pro Pro Pro Pro Pro His Ala Leu Gly Ser

195

200

205

Arg Gly Pro Pro Thr Pro Ala Pro Pro Gly Ala Pro Gly Gly Pro Ala
210 215 220

Cys Leu Gly Gly Thr Pro Gly Val Ser Ala Thr Ser Ser Ser Ala Ser
225 230 235 240

Ser Ser Thr Ser Ser Ser Val Ala Glu Val Gly Val Gly Ala Gly Gly
245 250 255

Lys Arg Pro Gly Ser Val Ser Ser Thr Asp Gln Glu Arg Glu Leu Lys
260 265 270

Glu Lys Gln Arg Asn Ala Glu Ala Leu Ala Glu Leu Ser Glu Ser Leu
275 280 285

Arg Asn Arg Ala Glu Glu Trp Ala Ser Lys Pro Lys Met Val Arg Asp
290 295 300

Thr Leu Leu Thr Leu Ala Gly Cys Thr Pro Tyr Glu Val Arg Phe Lys
305 310 315 320

Lys Asp His Ser Leu Leu Gly Arg Val Phe Ala Phe Asp Ala Val Ser
325 330 335

Lys Pro Gly Met Asp Tyr Glu Leu Lys Leu Phe Ile Glu Tyr Pro Thr
340 345 350

Gly Ser Gly Asn Val Tyr Ser Ser Ala Ser Gly Val Ala Lys Gln Met
355 360 365

Tyr Gln Asp Cys Met Lys Asp Phe Gly Arg Gly Leu Ser Ser Gly Phe
370 375 380

Lys Tyr Leu Glu Tyr Glu Lys Lys His Gly Ser Gly Asp Trp Arg Leu
385 390 395 400

Leu Gly Asp Leu Leu Pro Glu Ala Val Arg Phe Phe Lys Glu Gly Val
405 410 415

Pro Gly Ala Asp Met Leu Pro Gln Pro Tyr Leu Asp Ala Ser Cys Pro
420 425 430

Met Leu Pro Thr Ala Leu Val Ser Leu Ser Arg Ala Pro Ser Ala Pro
435 440 445

Pro Gly Thr Gly Ala Leu Pro Pro Ala Ala Pro Ser Gly Arg Gly Ala
450 455 460

Ala Ala Ser Leu Arg Lys Arg Lys Ala Ser Pro Glu Pro Pro Asp Ser
465 470 475 480

Ala Glu Gly Ala Leu Lys Leu Gly Glu Glu Gln Gln Arg Gln Gln Trp
485 490 495

Met Ala Asn Gln Ser Glu Ala Leu Lys Leu Thr Met Ser Ala Gly Gly
500 505 510

Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro Pro Pro Pro Pro Pro
515 520 525

Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro Pro Glu Ser Ala Pro
530 535 540

Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met Ser Val Ala Asp Thr
545 550 555 560

Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser Ser Val His Ser Thr
565 570 575

Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro Val Ser Pro Ala Ser
580 585 590

Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn Gly Asp Leu Asn Leu
595 600 605

Gln Val Ala Pro Pro Pro Pro Ser Ala His Pro Gly Met Asp Gln Val
610 615 620

His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala Asn Ser Gly Pro Leu
625 630 635 640

Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp Thr His Phe Val Gln
645 650 655

Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe Pro Cys Ser Arg Glu
660 665 670

Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val Tyr Cys Pro Ser Gly
675 680 685

Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro Trp Ala Phe Met Gln
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Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val Lys Val Lys Lys Glu
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Arg Asp Pro

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Thr Ser Thr Glu Gly Xaa Lys Ile Pro Met Thr Pro Thr Ser Ser Phe
35 40 45

Val Ser Pro Pro Pro Pro Thr Ala Ser Pro His Ser Asn Arg Thr Thr
50 55 60

Pro Pro Glu Ala Ala Gln Asn Gly Gln Ser Pro Met Ala Ala Leu Ile

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70

75

80

Leu Val Ala Asp Asn Ala Gly Gly Ser His Ala Ser Lys Asp Ala Asn
85 90 95

Gln Val His Ser Thr Thr Arg Arg Asn Ser Asn Ser Pro Pro Ser Pro
100 105 110

Ser Ser Met Asn Gln Arg Arg Leu Gly Pro Arg Glu Val Gly Gly Gln
115 120 125

Gly Ala Gly Asn Thr Gly Gly Leu Glu Pro Val His Pro Ala Ser Leu
130 135 140

Pro Asp Phe Ser Leu Ala Thr Ser Ala Pro Leu Cys Cys Thr Leu Cys
145 150 155 160

His Glu Arg Leu Glu Asp Asn His Phe Val Gln Cys
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<210> 34

<211> 197

<212> PRT

<213> Homo sapiens

<400> 34

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Pro His Ser Asn Arg Thr Thr Pro Pro Glu Ala Ala Gln Asn Gly Gln
20 25 30

Ser Pro Met Ala Ala Leu Ile Leu Val Ala Asp Asn Ala Gly Gly Ser
35 40 45

His Ala Ser Lys Asp Ala Asn Gln Val His Ser Thr Thr Arg Arg Asn
50 55 60

Ser Asn Ser Pro Pro Ser Pro Ser Ser Met Asn Gln Arg Arg Leu Gly
65 70 75 80

Pro Arg Glu Val Gly Gly Gln Gly Ala Gly Asn Thr Gly Gly Leu Glu
85 90 95

Pro Val His Pro Ala Ser Leu Pro Asp Ser Ser Leu Ala Thr Ser Ala
100 105 110

Pro Leu Cys Cys Thr Leu Cys His Glu Arg Leu Glu Asp Thr His Phe
115 120 125

Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe Pro Cys Ser
130 135 140

Arg Gln Ser Ile Lys Gln Gln Gly Ala Ser Gly Glu Val Tyr Cys Pro
145 150 155 160

Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro Trp Ala Phe
165 170 175

Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val Lys Val Lys
180 185 190

Lys Glu Arg Asp Ser
195

<210> 35
<211> 197
<212> PRT
<213> Homo sapiens

<400> 35

Met Thr Pro Thr Ser Ser Phe Val Ser Pro Pro Pro Thr Ala Ser
1 5 10 15

Pro His Ser Asn Arg Thr Thr Pro Pro Glu Ala Ala Gln Asn Gly Gln
20 25 30

Ser Pro Met Ala Ala Leu Ile Leu Val Ala Asp Asn Ala Gly Gly Ser
35 40 45

His Ala Ser Lys Asp Ala Asn Gln Val His Ser Thr Thr Arg Arg Asn
50 55 60

Ser Asn Ser Pro Pro Ser Pro Ser Ser Met Asn Gln Arg Arg Leu Gly
65 70 75 80

Pro Arg Glu Val Gly Gly Gln Gly Ala Gly Asn Thr Gly Gly Leu Glu

85

90

95

Pro Val His Pro Ala Ser Leu Pro Asp Ser Ser Leu Ala Thr Ser Ala
 100 105 110

Pro Leu Cys Cys Thr Leu Cys His Glu Arg Leu Glu Asp Thr His Phe
 115 120 125

Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe Pro Cys Ser
 130 135 140

Arg Gln Ser Ile Lys Gln Gln Gly Ala Ser Gly Glu Val Tyr Cys Pro
 145 150 155 160

Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro Trp Ala Phe
 165 170 175

Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val Lys Val Lys
 180 185 190

Lys Glu Arg Asp Ser
 195

<210> 36
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 36

Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro
 1 5 10 15

Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro
 20 25 30

Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met
 35 40 45

Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser
 50 55 60

Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro
 65 70 75 80

Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn
85 90 95

Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Pro Ser Ala His Pro
100 105 110

Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala
115 120 125

Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp
130 135 140

Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe
145 150 155 160

Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val
165 170 175

Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro
180 185 190

Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val
195 200 205

Lys Val Lys Lys Glu Arg Asp Pro
210 215

<210> 37
<211> 0
<212> DNA
<213> Homo sapiens

<400> 37
000

<210> 38
<211> 0
<212> DNA
<213> Homo sapiens

<400> 38
000

<210> 39
<211> 0
<212> DNA
<213> Homo sapiens

<400> 39
000

<210> 40
<211> 0
<212> DNA
<213> Homo sapiens

<400> 40
000

<210> 41
<211> 923
<212> DNA
<213> Homo sapiens

<400> 41
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caacacctag cctgagactt ggcggcgagg ctgctatcct gaactagctt ggtaagtgtt 120
gtgtcccgaa ccagcgtaga gagacctcgg accagccgcc ttgatgacag catccgcgtc 180
ctccttttca tcatctcagg gtgtccagca gccctccatc tacagcttct cccaaataac 240
cagaagcttg tttctcagca atggtgtggc cgccaacgac aaactccttc tgtccagcaa 300
tcgcatcacc gccattgtca atgcctcggg ggaagtggtc aacgtattct tcgagggcat 360
tcagtacata aagggtgctg ttaccgatgc tcgtgactcg cgtctctacg acttttttga 420
ccccattgct gatcttatcc acaccatcga tatgaggcag ggccgtacgc tgcgtgactg 480
catggctgga gtgagccgtt ccgcctcact gtgccttgcg tacctcatga aataccactc 540
catgtcgctg ctggacgccc atacatggac caagtcgcgc cgccecatca tccggcccaa 600
caacggcttt tgggaacagc tcatcaatta cgaattcaag ctgtttaata acaacaccgt 660
gcgcatgata aactcgccgg taggtaacat cctgacatc tatgagaagg acctacgtac 720
gatgatatca atgtaagcca tcccgccag cccctgacat ctgccatcga tcttgacca 780
agactgaact tgaacactga cattttgtta gtaaagaaaa ccggatgggt ccttgtaaa 840
gggcaagaaa aaagggaggg ggttgagggt ttgaacgtag taagccttac cttaatagaa 900
ttaaattcat gaaacataaa aca 923

<210> 42
<211> 190
<212> PRT
<213> Homo sapiens

<400> 42

Met Thr Ala Ser Ala Ser Ser Phe Ser Ser Ser Gln Gly Val Gln Gln
 1 5 10 15

Pro Ser Ile Tyr Ser Phe Ser Gln Ile Thr Arg Ser Leu Phe Leu Ser
 20 25 30

Asn Gly Val Ala Ala Asn Asp Lys Leu Leu Leu Ser Ser Asn Arg Ile
 35 40 45

Thr Ala Ile Val Asn Ala Ser Val Glu Val Val Asn Val Phe Phe Glu
 50 55 60

Gly Ile Gln Tyr Ile Lys Val Pro Val Thr Asp Ala Arg Asp Ser Arg
 65 70 75 80

Leu Tyr Asp Phe Phe Asp Pro Ile Ala Asp Leu Ile His Thr Ile Asp
 85 90 95

Met Arg Gln Gly Arg Thr Leu Leu His Cys Met Ala Gly Val Ser Arg
 100 105 110

Ser Ala Ser Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ser Met Ser
 115 120 125

Leu Leu Asp Ala His Thr Trp Thr Lys Ser Arg Arg Pro Ile Ile Arg
 130 135 140

Pro Asn Asn Gly Phe Trp Glu Gln Leu Ile Asn Tyr Glu Phe Lys Leu
 145 150 155 160

Phe Asn Asn Asn Thr Val Arg Met Ile Asn Ser Pro Val Gly Asn Ile
 165 170 175

Pro Asp Ile Tyr Glu Lys Asp Leu Arg Thr Met Ile Ser Met
 180 185 190

<210> 43
 <211> 570
 <212> DNA
 <213> Homo sapiens

<400> 43
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agcttctccc aaataaccag aagcttggtt ctcagcaatg gtgtggccgc caacgacaaa 120
 ctcttctgt ccagcaatcg catcacgcc attgtcaatg cctcggtgga agtgggcaac 180
 gtattcttcg agggcattca gtacataaag gtgcctgtta ccgatgetcg tgactcgcgt 240
 ctctacgact tttttgacct cattgetgat cttatccaca ccatcgatat gaggcagggc 300
 cgtacgctgc tgcaactgcat ggctggagtg agccgttcg cctcactgtg ccttgcgtag 360
 ctcatgaaat accactccat gtcgctgctg gacgccata catggaccaa gtcgcgcgc 420
 cccatcatcc ggccaacaa cggttttgg gaacagctca tcaattacga attcaagctg 480
 ttttaataaca acaccgtgcg catgatcaac tcgccggtag gtaacatccc tgacatctat 540
 gagaaggacc tacgtacgat gatatcaatg 570

<210> 44
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 44

Met Thr Ala Ser Ala Ser Ser Phe Ser Ser Ser Gln Gly Val Gln Gln
 1 5 10 15

Pro Ser Ile Tyr Ser Phe Ser Gln Ile Thr Arg Ser Leu Phe Leu Ser
 20 25 30

Asn Gly Val Ala Ala Asn Asp Lys Leu Leu Leu Ser Ser Asn Arg Ile
 35 40 45

Thr Ala Ile Val Asn Ala Ser Val Glu Val Val Asn Val Phe Phe Glu
 50 55 60

Gly Ile Gln Tyr Ile Lys Val Pro Val Thr Asp Ala Arg Asp Ser Arg
 65 70 75 80

Leu Tyr Asp Phe Phe Asp Pro Ile Ala Asp Leu Ile His Thr Ile Asp
 85 90 95

Met Arg Gln Gly Arg Thr Leu Leu His Cys Met Ala Gly Val Ser Arg
 100 105 110

Ser Ala Ser Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ser Met Ser
 115 120 125

Leu Leu Asp Ala His Thr Trp Thr Lys Ser Arg Arg Pro Ile Ile Arg
130 135 140

Pro Asn Asn Gly Phe Trp Glu Gln Leu Ile Asn Tyr Glu Phe Lys Leu
145 150 155 160

Phe Asn Asn Asn Thr Val Arg Met Ile Asn Ser Pro Val Gly Asn Ile
165 170 175

Pro Asp Ile Tyr Glu Lys Asp Leu Arg Met Met Ile Ser Met
180 185 190